Abstract

The systems and methods described herein relate to nucleic acid probes comprising a a pattern of universal and designate nucleotides, or 'gapped' probes, and the use of sets of gapped probes in sequencing by hybridization to determine the sequence of nucleic acid sequences. The inclusion of universal nucleotides in the probes allows for efficient and rapid sequencing of longer nucleotide sequences than can be sequenced using traditional probes. The systems and methods described herein also relate to apparatus for sequencing nucleic acids which include gapped probes, as well as computer systems capable of analyzing data generated using gapped probes in such apparatus.